

Filename : Phrixothrix vivianii lateral lanterns green light-eliciting
luciferase cDNA and deduced primary structure.
Sequence Size : 1746
Sequence Position: -25 - 1746

Translation Position: 1 - 1635;

Genetic Code : Universal (amino-acid residues are in 3 letter code)

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                                     -20      -10
                                     TCA GTG CAA GACT TTAG GG
                                     TCAGT GCAAGACTTTAGGG

      10      20      30      40      50
ATCAAAATGGAAGAAGAAAACATTAGGCATGGAGAGCGTCTCGTGATATAGTCCATCCT
  MetGluGluGluAsnIleArgHisGlyGluArgProArgAspIleValHisPro

      60      70      80      90     100     110
GGCTCGGCAGGACAACAATTATACCAATCATTGTATAAATTTGCATCTTTTCCTGAAGCA
GlySerAlaGlyGlnGlnLeuTyrGlnSerLeuTyrLysPheAlaSerPheProGluAla

     120     130     140     150     160     170
ATAATCGATGCTCATACAAATGAAGTAATATCATATGCTCAAATATTTGAAACCAGCTGC
IleIleAspAlaHisThrAsnGluValIleSerTyrAlaGlnIlePheGluThrSerCys

     180     190     200     210     220     230
CGCTTAGCTGTTAGTATAGAACAATATGGCTTGAATGAAAACAATGTTGTGGGTGTATGC
ArgLeuAlaValSerIleGluGlnTyrGlyLeuAsnGluAsnAsnValValGlyValCys

     240     250     260     270     280     290
AGTGAAAACAATATAAACTTTTTTAATCCTGTCCTTGCTGCTTTATACTTAGGAATACCA
SerGluAsnAsnIleAsnPhePheAsnProValLeuAlaAlaLeuTyrLeuGlyIlePro

     300     310     320     330     340     350
GTAGCAACATCAAATGATATGTACACAGATGGAGAGTTAACTGGTCATTTGAATATATCA
ValAlaThrSerAsnAspMetTyrThrAspGlyGluLeuThrGlyHisLeuAsnIleSer

     360     370     380     390     400     410
AAACCAACTATCATGTTTAGTTCAAAGAAAGCACTCCCGCTTATTCTGAGAGTACAGCAA
LysProThrIleMetPheSerSerLysLysAlaLeuProLeuIleLeuArgValGlnGln

     420     430     440     450     460     470
AATCTAAGTTTCATTAAAAAGTCGTAGTTATCGATAGCATGTACGACATTAAATGGCGTT
AsnLeuSerPheIleLysLysValValValIleAspSerMetTyrAspIleAsnGlyVal

     480     490     500     510     520     530
GAATGCGTATCTACCTTTGTTGCACGTTATACTGACCACACCTTTGATCCATTGTCATTT
GluCysValSerThrPheValAlaArgTyrThrAspHisThrPheAspProLeuSerPhe

     540     550     560     570     580     590
ACACCAAAGATTTTGATCCCCTTGAAAAAATCGCATTAATTATGTCATCATCTGGAACA
ThrProLysAspPheAspProLeuGluLysIleAlaLeuIleMetSerSerSerGlyThr
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FIG. 1A

600 610 620 630 640 650
ACTGGATTGCCTAAGGGTGTAGTACTGAGCCATAGAAGTCTAACTATAAGATTTCGTTTCAT
ThrGlyLeuProLysGlyValValLeuSerHisArgSerLeuThrIleArgPheValHis

660 670 680 690 700 710
AGCAGGGATCCCATTTTATGGCACTCGTACGGTTCCACAAACATCAATTCTTTCCTTAGTA
SerArgAspProIleTyrGlyThrArgThrValProGlnThrSerIleLeuSerLeuVal

720 730 740 750 760 770
CCGTTCCATCATGCCTTTGGAATGTTTACTACATTATCTTACTTTGTAGTAGGACTTAAG
ProPheHisHisAlaPheGlyMetPheThrThrLeuSerTyrPheValValGlyLeuLys

780 790 800 810 820 830
GTTGTAATGTTGAAGAAATTTGAGGGCGCACTTTTCTTAAAAACCATACAGAATTACAAA
ValValMetLeuLysLysPheGluGlyAlaLeuPheLeuLysThrIleGlnAsnTyrLys

840 850 860 870 880 890
ATCCCCACTATTGTAGTGGCCCCCTCCAGTTATGGTGTTTTTGGCTAAAGCCCATTAGTC
IleProThrIleValValAlaProProValMetValPheLeuAlaLysSerProLeuVal

900 910 920 930 940 950
GATCAATACGATTTATCGAGCTTAACGGAAGTTGCTACTGGAGGAGCTCCTTTAGGAAAA
AspGlnTyrAspLeuSerSerLeuThrGluValAlaThrGlyGlyAlaProLeuGlyLys

960 970 980 990 1000 1010
GATGTCGCAGAAGCAGTAGCAAGAGGTTGAAATTACCTGGAATCATACAAGGATATGGA
AspValAlaGluAlaValAlaLysArgLeuLysLeuProGlyIleIleGlnGlyTyrGly

1020 1030 1040 1050 1060 1070
TTAACTGAAACTTGCTGCGCTGTAATGATTACCCCTCATAATGCTGTGAAACAGGTTCA
LeuThrGluThrCysCysAlaValMetIleThrProHisAsnAlaValLysThrGlySer

1080 1090 1100 1110 1120 1130
ACTGGAAGACCCTTGCCATACATTAAAGCTAAAGTTTTAGATAACGCTACTGGGAAGGCG
ThrGlyArgProLeuProTyrIleLysAlaLysValLeuAspAsnAlaThrGlyLysAla

1140 1150 1160 1170 1180 1190
CTAGGACCAGGAGAAAGAGGCGAAATATGCTTTCAAAGTGAAATGATTATGAAAGGATAT
LeuGlyProGlyGluArgGlyGluIleCysPheGlnSerGluMetIleMetLysGlyTyr

1200 1210 1220 1230 1240 1250
TACACCAATCCGGAAGCAACTATTGATACTATTGACAAAGATGGTTGGCTTCATTCTGGA
TyrAsnAsnProGluAlaThrIleAspThrIleAspLysAspGlyTrpLeuHisSerGly

1260 1270 1280 1290 1300 1310
GATATTGGATATTACGACGAAGATGGAAATTTCTTTATAGTTGATCGATTGAAAGAACTT
AspIleGlyTyrTyrAspGluAspGlyAsnPhePheIleValAspArgLeuLysGluLeu

1320 1330 1340 1350 1360 1370
ATTAAATACAAGGGATATCAGGTTGCGCCTGCTGAACTGGAAAATCTGCTTTTACAACAT
IleLysTyrLysGlyTyrGlnValAlaProAlaGluLeuGluAsnLeuLeuLeuGlnHis

1380 1390 1400 1410 1420 1430
CCAAGTATTGCTGATGCGGGTGTACTGGAGTTCCGGACGAATTTGGTGGACAATTACCT
ProSerIleAlaAspAlaGlyValThrGlyValProAspGluPheGlyGlyGlnLeuPro

FIG. 1B

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1440      1450      1460      1470      1480      1490
GCTGCTTGTGTTGTGTTAGAAATCTGGCAAGACGCTGACTGAAAAGGAAGTTCAAGATTTT
AlaAlaCysValValLeuGluSerGlyLysThrLeuThrGluLysGluValGlnAspPhe

1500      1510      1520      1530      1540      1550
ATTGCAGCACAAGTCACTCCAACAAAGCATCTTCGAGGCGGTGTCGTATTTGTAGACAGT
IleAlaAlaGlnValThrProThrLysHisLeuArgGlyGlyValValPheValAspSer

1560      1570      1580      1590      1600      1610
ATTCCGAAAGGCCCTACTGGAAACTCATCAGAAAGGAGCTCCGAGAAATATTTGCCAG
IleProLysGlyProThrGlyLysLeuIleArgLysGluLeuArgGluIlePheAlaGln

1620      1630      1640
CGAGCACCAAATCAAATTATAAGTTCAATGTATTGCTTTAGTTCTAAAATGTATATAA
ArgAlaProLysSerLysLeu***

ACAAGTTTTAGAACCTAATACATTCAATACTAAACAAAAAAAAAAAAAAAAAAAAA
1740
AAAAAA
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FIG. 1C

Filename : PhREcDNA
Sequence Size : 1720
Sequence Position: -40 - 1760
Translation Position: 1 - 1638;
Genetic Code : Universal (amino-acid residues in 1 letter code)

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                -30      -20      -10
          GTGACAGTTTAGTTTCAGTAGAAGATTTTTTTTGAGATCAAA

      10      20      30      40      50      60
ATGGAAGAAGAAAACGTTGTGAATGGAGATCGTCCTCGTGATCTAGTTTTTCCTGGCACA
M E E E N V V N G D R P R D L V F P G T

      70      80      90     100     110     120
GCAGGACTACAATTATATCAATCATTATATAAATAATTCATATATTACTGACGGAATAATC
A G L Q L Y Q S L Y K Y S Y I T D G I I

     130     140     150     160     170     180
GATGCCCCATACCAATGAAGTAATATCATATGCTCAAATATTTGAAACCAGCTGCCGCTTG
D A H T N E V I S Y A Q I F E T S C R L

     190     200     210     220     230     240
GCAGTTAGTCTAGAAAAATATGGCTTGGATCAATAACAATGTTGTGGCAATATGCAGTGAA
A V S L E K Y G L D H N N V V A I C S E

     250     260     270     280     290     300
AACACATACACTTTTTTGGCCCTTTAATTGCTGCTTTATACCAAGGAATACCAATGGCA
N N I H F F G P L I A A L Y Q G I P M A

     310     320     330     340     350     360
ACATCAAATGATATGTACACAGAAAGGGAGATGATTGGCCATTTGAATATATCGAAACCA
T S N D M Y T E R E M I G H L N I S K P

     370     380     390     400     410     420
TGCCTTATGTTTTGTTCAAAGAAATCACTCCCATTATTCTGAAAGTACAAAAACATCTA
C L M F C S K K S L P F I L K V Q K H L

     430     440     450     460     470     480
GATTCCTTAAAAGAGTCATAGTCATTGATAGTATGTACGATATCAATGGCGTTGAATGC
D F L K R V I V I D S M Y D I N G V E C

     490     500     510     520     530     540
GTATTTAGCTTTGATTCACGTAATACTGATCAGCCTTTGATCCAGTGAAATTTAACCCA
V F S F D S R N T D H A F D P V K F N P

     550     560     570     580     590     600
AAAGAGTTTGATCCCTTGGAAAGAACCGCATTAATTATGACATCATCTGGAACAACTGGA
K E F D P L E R T A L I M T S S G T T G

     610     620     630     640     650     660
TTGCCTAAAGGGGTAGTAATAAGCCATAGAAGTATAACTATAAGATTCGTCCATAGCAGT
L P K G V V I S H R S I T I R F V H S S
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FIG. 2A

670 680 690 700 710 720
GATCCCATCTATGGTACTCGTATTGCTCCAGATACATCAATTCTTGCTATAGCACCGTTC
D P I Y G T R I A P D T S I L A I A P F

730 740 750 760 770 780
CATCATGCCTTTGGACTGTTTACTGCCTAGCTTACTTTCCAGTAGGACTTAAGATTGTA
H H A F G L F T A L A Y F P V G L K I V

790 800 810 820 830 840
ATGGTGAAGAAATTTGAGGGCGAATTCTTCTTAAAAACCATACAAAATTACAAAATCGCT
M V K K F E G E F F L K T I Q N Y K I A

850 860 870 880 890 900
TCTATTGTAGTTCCTCCTCCAATTATGGTATATTTGGCTAAAAGTCCATTAGTCGATGAA
S I V V P P P I M V Y L A K S P L V D E

910 920 930 940 950 960
TACAATTGCTCGAGCTTAACGGAAATTGCTAGTGGAGGCTCTCCTTTAGGAAGAGATATC
Y N C S S L T E I A S G G S P L G R D I

970 980 990 1000 1010 1020
GCAGATAAAGTAGCAAAGAGATTGAAAGTACATGGAATCCTACAAGGATATGGATTAAACC
A D K V A K R L K V H G I L Q G Y G L T

1030 1040 1050 1060 1070 1080
GAAACCTGCAGCGCTCTAATACTTAGCCCCAATGATCGAGAACTTAAAAAGGTGCAATT
E T C S A L I L S P N D R E L K K G A I

1090 1100 1110 1120 1130 1140
GGAACGCCTATGCCATATGTTCAAGTTAAAGTTATAGATATCAATACTGGGAAGGCGCTA
G T P M P Y V Q V K V I D I N T G K A L

1150 1160 1170 1180 1190 1200
GGACCAAGAGAAAAGGCGAATATGCTTCAAAAGTCAATGCTTATGAAAGGATATCAC
G P R E K G E I C F K S Q M L M K G Y H

1210 1220 1230 1240 1250 1260
AACATCCGCAAGCAACTCGTGATGCTCTTGACAAAGATGGTTGGCTTCATACTGGGGAT
N N P Q A T R D A L D K D G W L H T G D

1270 1280 1290 1300 1310 1320
CTTGGATATTACGACGAAGACAGATTTATCTATGTAGTTGATCGATTGAAAGAACTTATT
L G Y Y D E D R F I Y V V D R L K E L I

1330 1340 1350 1360 1370 1380
AAATATAAAGGATATCAGGTTTGGCGCTGCTGAACTGGAAAATCTGCTTTTACAACATCCA
K Y K G Y Q V A P A E L E N L L L Q H P

1390 1400 1410 1420 1430 1440
AATATTTCTGATGCGGGTGTATTGAATTCCGGACGAATTTGCTGGTCAATTACCTTTCC
N I S D A G V I E F R T N L L V N Y L S

1450 1460 1470 1480 1490 1500
GCGTGTGTTGTGTTAGAGCCTGGTAAGACAATGACCGAAAAGGAAGTTCAGGATTATATT
A C V V L E P G K T M T E K E V Q D Y I

FIG. 2B

1510	1520	1530	1540	1550	1560
GCAGAGCTAGTCACTACAACATAACATCTTCGAGGCGGTGTCGTATTTATAGATAGTATT					
A E L V T T T K H L R G G V V F I D S I					
1570	1580	1590	1600	1610	1620
CCAAAGGGCCCAACAGGAAACTCATGAGAAACGAACTCCGAGCAATATTTGCCCGGGAA					
P K G P T G K L M R N E L R A I F A R E					
1630	1640	1650	1660	1670	1680
CAGGCAAAATCAAATTATAAGCTCAATATATTGCTTTAGTTATAAAATGTATGTAATCA					
Q A K S K L *					
1690	1700	1710	1720		
AATTTTAGAACCTAATACATTCATTGAGAGCCTAAAAAA					

FIG. 2C

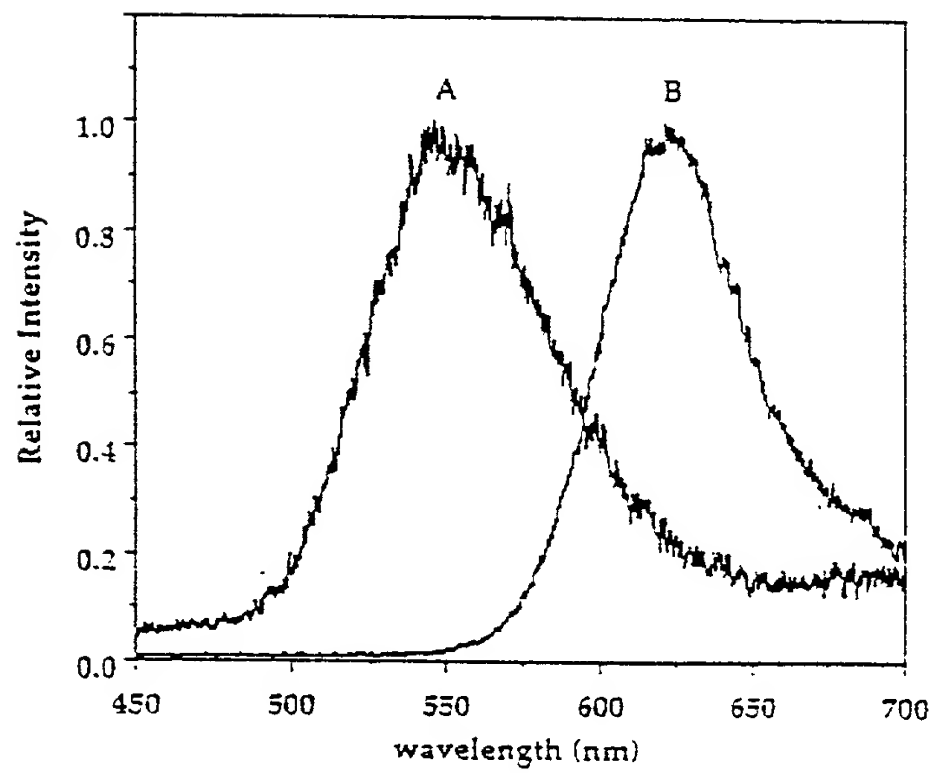


FIG. 3